

# SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> Novel Polypeptides, DNAs encoding the polypeptides, and utility of the Polypeptides

<130> Q79834

<140> 10/774,378

<141> 2004-02-10

<150> 09/380,276

<151> 1999-08-27

<150> JP 9-43143

<151> 1997-02-27

<150> PCT/JP98/00799

<151> 1997-02-27

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<170> PatentIn version 3.0

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(3/16)

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(5/16)

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atg gag tgt gtg cct tgt gga gac cct cct cct cct tac gaa ccg cac Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro His 110 115 120	488
tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc acg gcc tcc agc Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser Thr Ala Ser Ser 125 130 135	536
cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc gct ctg gcc acc Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala Thr 140 145 150 155	584
gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat tgt aag aga cag Val Leu Leu Ala Leu Ile Leu Cys Val Ile Tyr Cys Lys Arg Gln 160 165 170	632
ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca cag gac att cag Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser Gln Asp Ile Gln 175 180 185	680
tac aac ggc tct gag ctg tgc tgt ctt gac aga cct cag ctc cac gaa Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro Gln Leu His Glu 190 195 200	728
tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac tca gtg cag acc Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp Ser Val Gln Thr 205 210 215	776
tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt gag gag gcc tgc Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys Glu Glu Ala Cys 220 225 230 235	824
agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat tct gca gcc agt Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His Ser Ala Ala Ser 240 245 250	872
ctt cag gca aga aac gca ggc cca gcc ggg gag atg gtg ccg act ttc Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met Val Pro Thr Phe 255 260 265	920
ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt tca gat gcc tgg Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe Ser Asp Ala Trp 270 275 280	968
cct ctg atg cag aat ccc atg ggt ggt gac aac atc tct ttt tgt gac Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile Ser Phe Cys Asp 285 290 295	1016
tct tat cct gaa ctc act gga gaa gac att cat tct ctc aat cca gaa Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser Leu Asn Pro Glu 300 305 310 315	1064
ctt gaa agc tca acg tct ttg gat tca aat agc agt caa gat ttg gtt Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser Gln Asp Leu Val 320 325 330	1112
ggt ggg gct gtt cca gtc cag tct cat tct gaa aac ttt aca gca gct Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn Phe Thr Ala Ala 335 340 345	1160
act gat tta tct aga tat aac aac aca ctg gta gaa tca gca tca act Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu Ser Ala Ser Thr 350 355 360	1208

cag gat gca cta act atg aga agc cag cta gat cag gag agt ggc gct 1256  
 Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln Glu Ser Gly Ala  
 365 370 375

atc atc cac cca gcc act cag acg tcc ctc cag gta agg cag cga ctg 1304  
 Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Val Arg Gln Arg Leu  
 380 385 390 395

ggg tcc ctg tgaacacagc actgacttac agtagatcag aactctgttc 1353  
 Gly Ser Leu

ccagcataag atttggggga acctgatgag tttttttttt gcattctttaa taatttcttg 1413

tatgtttgtag agtatgtttt aaaataaatt tcaagtattt tttttaaaaa ctataaaaaa 1473

aaaaaaaaaa aaaaaaaaaa aaa 1496

<210> 8  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Origin: human bone marrow stromal cell line HAS303

<400> 8

Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu  
 -25 -20 -15 -10

Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly  
 -5 -1 1 5

Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro  
 10 15 20

Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe  
 25 30 35

Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe  
 40 45 50 55

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala  
 60 65 70

Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala  
 75 80 85

Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val  
 90 95 100

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro  
 (11/16)

105

110

115

Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser  
 120 125 130 135

Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser  
 140 145 150

Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr  
 155 160 165

Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser  
 170 175 180

Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro  
 185 190 195

Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp  
 200 205 210 215

Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys  
 220 225 230

Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His  
 235 240 245

Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met  
 250 255 260

Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe  
 265 270 275

Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile  
 280 285 290 295

Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser  
 300 305 310

Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser  
 315 320 325

Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn  
 330 335 340

Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu  
 345 350 355

Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln  
 (12/16)

360	365	370	375
Glu Ser Gly Ala	Ile Ile His Pro Ala	Thr Gln Thr Ser Leu	Gln Val
	380	385	390

Arg Gln Arg Leu Gly Ser Leu  
395

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<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<220>  
<221> misc\_feature  
<222> 27..35  
<223> n can be any nucleotide

<400> 9  
cgattgaatt ctagacctgc ctcgagnnnn nnnnn 35

<210> 10  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer OAF065

<400> 10  
agaaagatgg ctttaaaagt gctactag 28

<210> 11  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Aminod acid sequence of OAF065s

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Met Ala Leu Lys Val Leu Leu Glu Gln Glu Lys Thr Phe Phe Thr Leu  
1 5 10 15  
Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly  
20 25 30  
Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro  
35 40 45  
Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe  
50 55 60

(13/16)

Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe  
 65 70 75 80  
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala  
 85 90 95  
 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala  
 100 105 110  
 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr  
 115 120

<210> 12  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
 1 5 10 15  
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
 20 25 30  
 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45  
 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60  
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
 65 70 75 80  
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 85 90 95  
 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 100 105 110  
 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125  
 Lys Asn Gln Tyr  
 130

<210> 13  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 13  
 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
 1 5 10 15  
 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
 20 25 30  
 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln  
 35 40 45



Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro  
 50 55 60  
 Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro  
 65 70 75 80  
 Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His  
 85 90 95  
 Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly  
 100 105 110  
 Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg  
 115 120 125  
 Cys Lys Pro Asn Phe Phe  
 130